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SEA PYRUVATE DECARBOXYLASE

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L1 QUE PYRUVATE DECARBOXYLASE

FILE 'CAPLUS, BIOSIS, SCISEARCH, MEDLINE, EMBASE, BIOTECHNO, LIFESCI, PASCAL, DGENE, ESBIOBASE, BIOTECHDS' ENTERED AT 17:26:10 ON 24 APR 2003

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L2            52 S L1 AND THERMOSTAB?
L3        457722 S L2 AND YEAST OR SACCHARO?
L4            27 S L2 AND (YEAST OR SACCHARO?)
L5            10 DUP REM L4 (17 DUPLICATES REMOVED)
L6           116 S L1 AND (PDC5 OR PDC 5)
L7           114 S L6 AND (GENE OR CDNA OR CLON?)
L8            28 DUP REM L7 (86 DUPLICATES REMOVED)
L9             0 S L8 AND THERMOST?
L10            0 S L8 AND (OPTIM? TEMP?)
L11            2 S L8 AND TEMP?

=> log Y
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L5 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1979:401925 CAPLUS
DOCUMENT NUMBER: 91:1925
TITLE: The effects of the chemical surface structures of functionalized polystyrenes on the kinetic properties of immobilized **yeast pyruvate decarboxylase**
AUTHOR(S): Beitz, J.; Schellenberger, A.
CORPORATE SOURCE: Sekt. Biowiss., Martin-Luther-Univ. Halle-Wittenberg, Halle/Saale, 402, Ger. Dem. Rep.
SOURCE: Acta Biologica et Medica Germanica (1979), 37(9), 1399-411
CODEN: ABMGAJ; ISSN: 0001-5318
DOCUMENT TYPE: Journal
LANGUAGE: German
AB The influence of the loading d. of different functional groups and the length of suitable spacer structures on the kinetic properties of **yeast pyruvate decarboxylase** were investigated on identical polystyrene matrixes. At const. concns. of the fixed protein, both the specific activity and the storage stability of the immobilized enzymes increased with increasing concns. of the protein-binding C:O groups. The pH optimum and Km value were functions of the NH3+-content of the supports. Using 4 spacer resins with an equal content of spacer groups, it could be shown that the optimum time of coupling as well as the max. catalytic activity, storage stability, and **thermostability** depend on the length of the spacer structures. On the other hand, the mobility of an ESR marker fixed via the same spacers to the resin was not affected by the different spacer structures.

L5 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 2

ACCESSION NUMBER: 1999:436880 CAPLUS
DOCUMENT NUMBER: 131:210818
TITLE: Effects of substitution of tryptophan 412 in the substrate activation pathway of **yeast pyruvate decarboxylase**
AUTHOR(S): Li, Haijuan; Jordan, Frank
CORPORATE SOURCE: Departments of Chemistry and Biological Sciences and Program in Cellular and Molecular Biodynamics, Rutgers the State University, Newark, NJ, 07102, USA
SOURCE: Biochemistry (1999), 38(31), 10004-10012
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Oligonucleotide-directed site-specific mutagenesis was carried out on **pyruvate decarboxylase** (EC 4.1.1.1) from **Saccharomyces** cerevisiae at Trp-W412, located on the putative substrate activation pathway and linking Glu-91 on the .alpha. domain with Trp-412 on the .gamma. domain of the enzyme. Whereas Cys-221 on the .beta. domain is the residue at which substrate activation is triggered, that information, via the substrate bound at Cys-221, is transmitted to His-92 on the .alpha. domain, across the domain divide from Cys-221, thence to Glu-91 on the .alpha. domain, and then on to Trp-412 on the .gamma. domain and to the active site thiamin diphosphate (ThDP) located at the interface of the .alpha. and .gamma. domains. Here, substitution at Trp-412 with Phe and Ala was carried out, resulting in active enzymes with specific activities about 4- and 10-fold lower than that of the wild-type enzyme. Even though Trp-412 interacted with Glu-91 and His-115 via a main chain H-bond donor and acceptor, resp., there was clear evidence for the importance of the indole side-chain of Trp-412 from a variety of expts.: **thermostability**, fluorescence quenching, the binding consts. of ThDP, and CD spectroscopy, in addn. to conventional steady-state kinetic measurements. Whereas the substrate activation was still prominent in the W412F variant, its level was very much reduced in the W412A variant, signaling that the size of the side-chain was also important in positioning the amino acids surrounding the active center to achieve substrate activation. The fluorescence studies demonstrated that Trp-412 is a relatively minor contributor to the well-documented fluorescence of apopyruvate decarboxylase in its native state. The information about the Trp-412 variants provided strong addnl. support for the putative substrate activation pathway from Cys-221 .fwdarw. His-92 .fwdarw. Glu-91 .fwdarw. Trp-412 .fwdarw. Gly-413 .fwdarw. ThDP. The accumulating evidence for the central role of the .beta. domain in stabilizing the overall structure was summarized.

L8 ANSWER 23 OF 28 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 15
ACCESSION NUMBER: 1990:453406 CAPLUS
DOCUMENT NUMBER: 113:53406
TITLE: Autoregulation may control the expression of yeast **pyruvate decarboxylase** structural **genes** PDC1 and **PDC5**
AUTHOR(S): Hohmann, Stefan; Cederberg, Hakan
CORPORATE SOURCE: Inst. Mikrobiol., TH Darmstadt, Darmstadt, D-6100, Germany
SOURCE: European Journal of Biochemistry (1990), 188(3), 615-21
CODEN: EJBCAI; ISSN: 0014-2956
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors deleted the **pyruvate decarboxylase** structural **gene** PDC1 from the genome of Saccharomyces cerevisiae. The pdc1 deletion mutants had **pyruvate decarboxylase** activity due to the presence of a second structural **gene**. This **gene**, **PDC5**, was **cloned** and sequenced. The predicted amino acid sequences of PDC1 and **PDC5** are 88% identical. Deletion of **PDC5** did not cause any decrease in the specific **pyruvate decarboxylase** activity, while pdc1 deletion mutants had 80% of the wild-type activity. Deletion mutants lacking both PDC1 and **PDC5** did not show any detectable **pyruvate decarboxylase** activity in vitro and were unable to ferment glucose. This indicates that PDC1 and **PDC5** are the only structural **genes** for **pyruvate decarboxylase** in yeast. The **PDC5** isoenzyme showed a slightly higher Km value for its substrate pyruvate than the PDC1 product (**PDC5**: Km = 8 mM; PDC1: Km = 5 mM), as measured in a crude ext. of pdc1 and **pdc5** deletion mutants, resp. **PDC5** Is only expressed in pdc1 deletion mutants. No mRNA transcribed from **PDC5** could be detected in wild-type cells. Thus, in addn. to the control by glucose induction, **pyruvate decarboxylase** activity seems to be subject to autoregulation. Similar phenomena have been described previously for tubulin, histones, and a ribosomal protein but not for metabolic enzymes.

L8 ANSWER 21 OF 28 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:161969 CAPLUS
DOCUMENT NUMBER: 118:161969
TITLE: Structure and expression of yeast **pyruvate decarboxylase** structural **genes**
AUTHOR(S): Hohmann, Stefan
CORPORATE SOURCE: Inst. Mikrobiol., Tech. Hochsch. Darmstadt, Darmstadt, D-6100, Germany
SOURCE: Biochem. Physiol. Thiamin Diphosphate Enzymes, Proc. Int. Meet. Funct. Thiamin Diphosphate Enzymes (1991), Meeting Date 1990, 106-14. Editor(s): Bisswanger, Hans; Ullrich, Johannes. VCH: Weinheim, Fed. Rep. Ger.
CODEN: 57LOA7
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Three structural **genes** for pyruvate tdecarboxylase named PDC1, **PDC5**, and PDC6 have been identified in the haploid genome of Saccharomyces cerevisiae and the DNA sequences of these **genes** have been detd. All three **genes** code for primary translation products of 563 amino acids and the deduced amino acid sequences are 88% (PDC1-**PDC5**), 83% (PDC1-PDC6), 80% (**PDC5**-PDC6) and 78% (PDC1-**PDC5**-PDC6) identical. The differences in the primary structure are unevenly distributed over the protein sequence. The three structural **genes** are differentially expressed. In wild-type yeast strains growing on glucose, the product of PDC1 is at least six times more abundant than the **PDC5** product. Deletion mutants lacking both the PDC1 and the **PDC5 gene** have no detectable **pyruvate decarboxylase** activity in crude exts. This indicates that the third structural **gene**, PDC6, is not expressed during growth on glucose. However, expression of PDC6 was obsd. in certain mutants where PDC6 had come under the control of the PDC1 promoter by a spontaneous rearrangement. In mutants where the PDC1 **gene** has been deleted, the expression of **PDC5** is enhanced between 4-5 fold, apparently to compensate for the loss of the PDC1 structural **gene**. This phenomenon points to an involvement of **pyruvate decarboxylase** in the regulation of its own synthesis.

L5 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1995:937941 CAPLUS
DOCUMENT NUMBER: 124:3896
TITLE: The enzyme properties of **pyruvate decarboxylase** modified with an amylose derivative
AUTHOR(S): Ohba, Hideki; Yasuda, Seiji; Hirosue, Hideharu; Yamasaki, Nobuyuki
CORPORATE SOURCE: Mater. Chem. Dep., Kyushu Natl. Ind. Res. Inst., Tosu, 841, Japan
SOURCE: Kyushu Kogyo Gijutsu Kenkyusho Hokoku (1995), 55, 3423-30
CODEN: KKOHE5; ISSN: 1340-3958
PUBLISHER: Kyushu Kogyo Gijutsu Kenkyusho
DOCUMENT TYPE: Journal
LANGUAGE: English

AB An amylose-glycylglycine adduct (AG) was covalently attached to **pyruvate decarboxylase** (PyDC) from brewer's **yeast**, and some properties of the resulting conjugate (AG-PyDC) were studied with regard to **thermostability**. The conjugate was prepd. by modification of PyDC with the N-hydroxysuccinimide ester of AG (AG-ONSu), and purified by gel filtration on a Bio gel P-199 column. Anal. data indicated that in the conjugate, 30 out of 68 amino groups in the PyDC mol. were modified with AG-ONSu and the main chain configuration of PyDC remained unchanged. By conjugation with AG the optimum temp. of the activity of PyDC changed from 35.degree. to 40.degree.. The conjugate showed a greater resistance than PyDC to inactivation by heat treatment: after treatment of the samples at 45.degree. for 20 min, AG-PyDC retained 80% of the activity, while the activity of native PyDC was only 25% of that of the untreated sample. It is suggested that AG-ONSu can be advantageously used for stabilization of the thermolabile enzyme, PyDC.

L6 ANSWER 4 OF 7 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2001-16051 BIOTECHDS
TITLE: Gram-positive bacteria for producing ethanol are transformed with a heterologous gene encoding pyruvate-decarboxylase or a functional equivalent and have solely **native** **alcohol-dehydrogenase** function;
plasmid pFC1-mediated Zymomonas mobilis or Saccharomyces cerevisiae enzyme gene transfer and expression in **Bacillus** sp. and L-lactic acid production
AUTHOR: Green E; Baghaei-Yazdi N; Javed M
PATENT ASSIGNEE: Elsworth-Biotechnology
LOCATION: Surrey, UK.
PATENT INFO: WO 2001049865 12 Jul 2001
APPLICATION INFO: WO 2001-GB36 5 Jan 2001
PRIORITY INFO: US 2000-177199 21 Jan 2000; GB 2000-185 6 Jan 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2001-496722 [54]
AB A Gram-positive bacterium (I, **Bacillus** stearothermophilus, **Bacillus** calvodex, **Bacillus** caldotenax, **Bacillus** thermoglucosidasius, **Bacillus** coagulans, **Bacillus** thermodenitrificans and **Bacillus** caldolyticus) transformed with a gene encoding Zymomonas mobilis or Saccharomyces cerevisiae pyruvate-decarboxylase (pdc, EC-4.1.1.1), with 300 bp DNA sequence fully defined, or a functional equivalent is claimed. Also claimed are: a method for producing ethanol; a method for producing L-lactic acid; a nucleic acid molecule containing the lactate-dehydrogenase promoter region of strain LN (NCIMB-41038); and plasmid pFC1. In an example, plasmid pFC1-PDC1 was transformed into Bacillis sp. TN and cultured in culture medium containing JSD supplemented with 50 mM PIPES buffer and 2% glucose at 54 deg for 24 hr. The TN-P3 strain was shown to produce 39.5 mM ethanol. The above can be used for producing ethanol and at high temp. and for producing L-lactic acid. (30pp)